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**FIG. 1 Promyostatin**

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1   MQKLQLCVYI YLFMLIVAGP VDLNENSEQK ENVEKEGLCN 40
41  ACTWRQNTKS SRIEAIKIQI LSKLRLETAP NISKDVIRQL 80
81  LPKAPPLREL IDQYDVQRDD SSDGSLEDDD YHATTETIIT 120
121 MPTESDFLMQ VDGKPKCCFF KFSSKIQYNK VVKAQLWIYL 160
161 RPVETPTTVF VQILRLIKPM KDGTRYTGIR SLKLDMNPGT 200
201 GIWQSIDVKT VLQNLWKQPE SNLGIEIKAL DENGHD LAVT 240
241 FPGPGEDGLN PFLEVKVTDT PKRSRRDFGL DCDEHSTESR 280
281 CCRYPLTVDF EAFGWDWIIA PKRYKANYCS GECEFVFLQK 320
321 YPHTHLVHQA NPRGSAGPCC TPTKMSPINM LYFNGKEQII 360
361 YGKIPAMVVD RCGCS 376 (SEQ ID NO:1)

```

**FIG. 2 Mature Myostatin (Human, murine, rat, chicken)**

```

1   DFGLDCDEHS TESRCCRYPL TVDFEAFGWD WIIAPKRYKA 40
41  NYCSGECEFEV FLQKYPHTHL VHQANPRGSA GPCCTPTKMS 80
81  PINMLYFNGK EQIIYGKIPA MVVDRCGCS 109 (SEQ ID NO:2)

```

**FIG. 3 Myostatin Homology with GDF-11**

```

Myostatin DFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYK
Consensus -+GLDCDEHS+ESRCCRYPLTVDFEAFGWDWIIAPKRYK
GDF-11    NLGLDCDEHSSESRCRYPLTVDFEAFGWDWIIAPKRYK

```

```

Myostatin ANYCSGECEFEVFLQKYPHTHLVHQANPRGSAGPCCTPTK
Consensus ANYCSG+CE++F+QKYPHTHLV-QANPRGSAGPCCTPTK
GDF-11    ANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTK

```

```

Myostatin MSPINMLYFNGKEQIIYGKIPAMVVDRCGCS 109 (SEQ ID NO:2)
Consensus MSPINMLYFN-K+QIIYGKIP+MVVDRCGCS (SEQ ID NO:39)
GDF-11    MSPINMLYFNDKQQIIYGKIPGMVVDRCGCS 108 (SEQ ID NO:40)

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Figure 4 Fab Light Chain Variable Region Alignment

<u>Fab</u>	1		<u>CDR1</u>	40
3	QIVLTQSPAI	MSASPGEKVT	MTCSASSSIS	YMHWYQQKPG
5	QVVLTTQSPAI	MSASLGEKVT	MTCSASSSVH	YMHWYQQKSG
7	QIVLTQSPAI	MSASPGEKVT	MTCSASSSIS	YMHWYQQKPG
8	QIVLTQSPAI	MSASPGEKVT	MTCSASSSVS	YMHWYQQKSG
9	QIVLTQSPAI	MSASPGEKVT	MTCSASSSVS	YMHWYQQKSG
10	QVVLTTQSPAI	MSASPGEKVT	MTCSASSSIS	YMHWYQQKPG
11	QIVLTQSPAI	MSASPGEKVT	MTCSASSSIS	YMHWYQQKPG
12	QVVLTTQSPAI	MSASPGEKVT	MTCSASSSVY	YMHWYQQRSG
14	QIVLTQSPAI	MSASPGEKVT	MTCSASSSVS	YMHWYQQKPG
15	QIVLTQSPAI	MSASPGEKVT	MTCSASSSIN	YMHWYQQKSG
	*	* *	**	**
<u>Fab</u>	41	<u>CDR2</u>		80
3	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
5	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
7	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
8	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
9	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
10	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
11	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
12	ASPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
14	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
15	TSPKRWIYDT	SKLASGVPAR	FSGSGSGTSY	SLTISSMEAE
	*			
<u>Fab</u>	81	<u>CDR3</u>		108
3	DAATYYCQQW	YSNPLTFGAG	TKLELKRAD	(SEQ ID NO:3)
5	DAATYYCQQW	SSNPLTFGAG	TKLELKRAD	(SEQ ID NO:4)
7	DAATYYCQQW	YSNPLTFGAG	TKLELKRAD	(SEQ ID NO:3)
8	DAATYYCQQW	SSNPLTFGAG	TKLELKRAD	(SEQ ID NO:5)
9	DAATYYCQQW	SRNPLTFGAG	TKLELKRAD	(SEQ ID NO:6)
10	DAATYYCQQW	YSNPLTFGAG	TKLELKRAD	(SEQ ID NO:7)
11	DAATYYCQQW	NSNPLTFGAG	TKLELKRAD	(SEQ ID NO:8)
12	DAATYYCQQW	TYNPLTFGAG	TKLELKRAD	(SEQ ID NO:9)
14	DAATYYCQQW	YSNPLTFGAG	TKLELKRAD	(SEQ ID NO:10)
15	DAATYYCQQW	NSNPLTFGGG	TKLELKRAD	(SEQ ID NO:11)
		** *		

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Figure 5 Fab Heavy Chain Variable Region Alignment

<u>Fab</u>	1	<u>CDR1</u>				40
3	QVTLKESGPG	ILQSSQTL	SL	TCSLSG	FSLR	TSGMSVSWIR
5	QVTLKESGPG	ILQSSQTL	SL	TCSFSG	FSLR	TSGMSVSWIR
7	QVTLK-SGPG	ILQSSQTL	TL	TCSLSG	FSLT	TSGMIVSWIR
8	QVTLKESGPG	ILQSSQTL	SL	TCSLSG	FSLR	TSGMSVSWIR
9	QVTLKESGPG	ILQSSQTL	SL	TCSVSG	FSLR	TSGMSVSWIR
10	QVTLKESGPG	ILQPSQTL	SL	TCSLSG	FSLR	TSGMSVSWIR
11	QVTLKESGPG	ILQSSQTL	SL	TCSLSG	FSLR	TSGMSVSWIR
12	QVTLKESGPG	MLQSSQTL	SL	TCSLSG	FSLR	TSGMSVSWIR
14	QVTLKESGPG	ILQSSQTL	SL	TCSLSG	FSLR	TSGMSVSWIR
15	QVTLKESGPG	ILQSSQTL	SL	TCSLSG	FSLR	TSGMSVSWIR
	*	*	*	*	*	*
<u>Fab</u>	41	<u>CDR2</u>				80
3	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV		
5	QSSGKGLEWL	AHIYWDDDKR	YNPSLRSRLT	ISKDTSRNQV		
7	QSSGRGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV		
8	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV		
9	QPSGKGLEWL	AHIYWDDDKR	YNPSLKSRLT	ISKDTSRNQV		
10	QSSGKGLEWL	AHIYWDDDER	YNPSLRNRLT	ISKDTLRNQV		
11	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV		
12	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV		
14	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV		
15	QSSGKGLEWL	AHIYWDDDKR	YNPSLRNRLT	ISKDTLRNQV		
	*	*	**	*		
<u>Fab</u>	81	<u>CDR3</u>				
3	FLKITSVGTADTATYYCARRA	ITTVIGGGTMDYWGQGT	SVTVSS			
5	FLKITSVDTADTATYYCARRG	ITTVLGGGTMDYWGQGT	SVTVSS			
7	FLWISSVGTADTATYYCARRA	ITTVIGGGTMDYWGQGT	SVTVSS			
8	FLKITSVGTADTATYYCARRA	ITTVIGGGTMDYWGQGT	SVTVSS			
9	FLKITSVDTADTATYYCARRA	ITTVLGGGTMDYWGQGT	SVTVSS			
10	FLKITSVGTADTATYYCARRA	ITTVIGGGTMDYWGQGT	SVTVSS			
11	FLKITSVGTADTATYYCARRA	ITTVIGGGTMDYWGQGT	SVTVSS			
12	FLKITSVGTADTATYYCARRA	ITTVIGGGTMDYWGQGT	SVTVSS			
14	FLKITSVGTADTATYYCARRA	ITTVIGGGTMDYWGQGT	SVTVSS			
15	FLKITSVGTADTATYYCARRA	ITTVIGGGTMDYWGQGT	SVTVSS			
	* * *	*	*			
3	(SEQ ID NO:12)					
5	(SEQ ID NO:13)					
7	(SEQ ID NO:14)					
8	(SEQ ID NO:12)					
9	(SEQ ID NO:15)					
10	(SEQ ID NO:17)					
11	(SEQ ID NO:12)					
12	(SEQ ID NO:16)					
14	(SEQ ID NO:12)					
15	(SEQ ID NO:12)					